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OM protein - protein search, using sw model

Run on: December 16, 2005, 15:16:35 ; Search time 7.58967 Seconds
2484.756 Million cell updates/sec

Title: US-09-272-809-9

Perfect score: 1024

Sequence: 1 KLA
VRAISRLQLP
GGD
IKA...QAFGQLQMBLQLASQALEK 196

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Searched:

phytochrome B - Arabidopsis thaliana

N;Alternate names: Protein F15J5_100

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 31-Dec-2004

C;Accession: S46313; T14813; S41912

R;Clack, T.; Mathews, S.; Sharrock, R.A.

Plant Mol. Biol. 25, 413-427, 1994

A;Title: The phytochrome apoprotein family in Arabidopsis is encoded by five genes: the

A;Reference number: S46312; MUID:94325466; PMID:8043367

A;Accession: S46313

A;Molecule type: DNA

A;Residues: 1-1112 <CLAA>

A;Cross-references: UNIPROT:P42498; UNIPARC:UPI0000131A6B; EMBL:AL110123; GSPDB:GN00062; ATSP:R15J5_100

R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, August 1999

A;Reference number: Z15120

A;Accession: T14813

A;Molecule type: DNA

A;Cross-references: UNIPARC:UPI0000131A6B; EMBL:AL110123; GSPDB:GN00062; ATSP:R15J5_100

A;Experimental source: cultivar Columbia; BAC clone F15J5

C;Genetics:

A;Gene: PhyB; ATSP:R15J5_100

A;Residues: 1-1112 <BEV>

A;Cross-references: UNIPARC:UPI0000131A6B; EMBL:AL110123; GSPDB:GN00062; ATSP:R15J5_100

A;Experimental source: cultivar Columbia; BAC clone F15J5

C;Position: 4

A;Introns: 665/1; 934/2; 1032/2

C;Superfamily: phytochrome, conventional type; phytochrome homology

C;Keywords: chromoprotein; photoreceptor; phytochromobilin

P;63-569;Domain: phytochrome homology <PHT>

P;322/Binding site: phytochromobilin (cys) (covalent) #status predicted

Query Match 100.0% Score 1024; DB 2; Length 1112;

Best Local Similarity 100.0% Pred. No. 5.5e-93; Indels 0; Missmatches 0; Gaps 0;

Matches 196; Conservative 0; #status predicted

Qy 1 KLA
VRAISRLQLP
GGD
IKA...QAFGQLQMBLQLASQALEK 196Db 201 KLA
VRAISRLQLP
GGD
IKA...QAFGQLQMBLQLASQALEK 196Qy 61 EPI
LGHLHYPATD
IPOAARFLFKONR
VRMICDCNATP
VKVQSEELK
RPLCLVNSTL
RAPH 120Db 261 EPI
LGHLHYPATD
IPOAARFLFKONR
VRMICDCNATP
VKVQSEELK
RPLCLVNSTL
RAPH 320Qy 121 GCH
TQYMAN
GSGV
ASLAL
AIVV
KGDSS
KLGIV
YGHCS
SPRY
YFPL
YACB
FIMQAFG 180Db 321 GCH
TQYMAN
GSGV
ASLAL
AIVV
KGDSS
KLGIV
YGHCS
SPRY
YFPL
YACB
FIMQAFG 380Qy 181 LQLQ
NBLQ
LQASQ
ALEK 196Db 381 LQLQ
NBLQ
LQASQ
ALEK 396

RESULT 1

S46313

phytochrome B - Arabidopsis thaliana

N;Alternate names: Protein F15J5_100

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 31-Dec-2004

C;Accession: S46313; T14813; S41912

R;Clack, T.; Mathews, S.; Sharrock, R.A.

Plant Mol. Biol. 25, 413-427, 1994

A;Title: The phytochrome apoprotein family in Arabidopsis is encoded by five genes: the

A;Reference number: S46312; MUID:94325466; PMID:8043367

A;Accession: S46313

A;Molecule type: DNA

A;Residues: 1-1112 <CLAA>

A;Cross-references: UNIPROT:P42498; UNIPARC:UPI0000131A6B; EMBL:AL110123; GSPDB:GN00062; ATSP:R15J5_100

R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, August 1999

A;Reference number: Z15120

A;Accession: T14813

A;Molecule type: DNA

A;Cross-references: UNIPARC:UPI0000131A6B; EMBL:AL110123; GSPDB:GN00062; ATSP:R15J5_100

A;Experimental source: cultivar Columbia; BAC clone F15J5

C;Position: 4

A;Introns: 665/1; 934/2; 1032/2

C;Superfamily: phytochrome, conventional type; phytochrome homology

C;Keywords: chromoprotein; photoreceptor; phytochromobilin

P;63-569;Domain: phytochrome homology <PHT>

P;322/Binding site: phytochromobilin (cys) (covalent) #status predicted

Query Match 100.0% Score 1024; DB 2; Length 1112;

Best Local Similarity 100.0% Pred. No. 5.5e-93; Indels 0; Missmatches 0; Gaps 0;

Matches 196; Conservative 0; #status predicted

Qy 1 KLA
VRAISRLQLP
GGD
IKA...QAFGQLQMBLQLASQALEK 196Db 201 KLA
VRAISRLQLP
GGD
IKA...QAFGQLQMBLQLASQALEK 196Qy 61 EPI
LGHLHYPATD
IPOAARFLFKONR
VRMICDCNATP
VKVQSEELK
RPLCLVNSTL
RAPH 120Db 261 EPI
LGHLHYPATD
IPOAARFLFKONR
VRMICDCNATP
VKVQSEELK
RPLCLVNSTL
RAPH 320Qy 121 GCH
TQYMAN
GSGV
ASLAL
AIVV
KGDSS
KLGIV
YGHCS
SPRY
YFPL
YACB
FIMQAFG 180Db 321 GCH
TQYMAN
GSGV
ASLAL
AIVV
KGDSS
KLGIV
YGHCS
SPRY
YFPL
YACB
FIMQAFG 380Qy 181 LQLQ
NBLQ
LQASQ
ALEK 196Db 381 LQLQ
NBLQ
LQASQ
ALEK 396

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1024	100.0	1112	2	S46313		Phytochrome B - Arabidopsis thaliana (mouse-ear cress)
2	840.5	82.1	1131	2	T07701		phytochrome - Ar
3	836	81.6	1135	2	T16973		phytochrome - Scot
4	828	80.9	1132	2	T03668		phytochrome - cu
5	806	78.7	1039	2	T14802		phytochrome - co
6	802	78.4	1172	1	FKMUB		phytochrome - so
7	794.5	77.5	1171	2	S14065		phytochrome - Ar
8	785	76.7	1142	2	S62714		phytochrome - ri
9	783	76.5	1164	2	B71429		phytochrome D - M
10	772	75.4	1156	2	T07756		phytochrome B - Ar
11	765.5	74.8	1136	2	T14842		phytochrome - B
12	763.5	74.6	577	2	S58130		phytochrome - B
13	763.5	74.6	1129	2	S28431		phytochrome B - po
14	747	72.9	1134	2	S31280		phytochrome - Mart
15	746	72.9	368	2	T07496		phytochrome - Doug
16	740.5	72.3	1132	2	T07205		phytochrome - moss
17	734.5	71.7	1135	2	T14803		phytochrome C - BO
18	723.5	70.7	1303	1	S27396		phytochrome / prot
19	717.5	70.1	211	2	S62720		phytochrome B1 - S
20	707	69.0	210	2	S62721		phytochrome B2 - S
21	706	68.9	1111	1	FKMUC		phytochrome C - Ar
22	687	67.1	1465	2	T30891		PHY3 Protein - mai
23	672	65.6	1122	1	FKMUA		phytochrome A - Ar
24	672	65.6	1122	2	D86229		phytochrome A / imp
25	671.5	65.4	1123	2	S20497		phytochrome A - po
26	669.5	65.4	1129	2	A29631		phytochrome 3 - oa
27	668.5	65.3	495	2	S00098		phytochrome 5 - oa
28	668	65.2	1129	2	S52631		phytochrome A - pa
29	666.5	65.1	1129	2	S00097		phytochrome 4 - oa

RESULT 2

T09701 Scotch pine
C:Species: *Pinus sylvestris* (Scotch pine)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
C:Accession: T09701
R:Wiesmann-Birndorf, C. M.; Kolukisaoglu, H. U.
R:Submitted to the EMBL Data Library, March 1996
A:Reference numbers: Z16826
A:Accession: T09701
A:Status: preliminary; translated from GB/EMBL/DDJB
A:Molecule type: mRNA
A:Residues: 1-1131 <WIB>
A:Cross-references: UNIPROT:Q41046; UNIPARC:UPI0000131A71; EMBL:X96738; NID:91237083
A:Experimental source: isolate P8A 5.1
C:Superfamily: phytochrome, conventional type; phytochrome homology
C:Keywords: chromoprotein; photoreceptor; phytochromobilin
F:75-587/Domain: phytochrome homology <PHY>
F:332/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match Score 840.5; DB 2; Length 1131;
Best Local Similarity 78.0%; Pred. No. 8.3e-75;
Matches 160; Conservative 15; Mismatches 21; Indels 9; Gaps 1;

Qy 1 KLAVALRISRLQSLPGDIGALCDTVDYQRLTGDRWVYQFEDDHGEVSEIRSDL 60
Db 211 KLAVALRISLQLSPCGDVLCDTVDYQRLTGDRWVYKFEDHEGEVSEIRSDL 270
Qy 61 EPYLGLHYPATDIPQAARFLFKONVRMIDCNATPVQVOSBELKRPCLVNSTRAPL 120
Db 271 EPYLGLHYPATDIPQAARFLFKONVRMIDCNATPVQVOSBELMOPCLVGSTPSAPL 330
Qy 121 GCHTOQMAMGVSASLAIIVVKGD-----SSKLWGLVGHCSPRYVPPFLRYA 171
Db 331 GCHQYQMAMGTSRSLMAVITNGNDDEGGSGRNSMKLWGLVYVCHHTSPRAVPPFLRYA 390
Qy 172 CEFLMQAFGLQLOMELQASLQAK 196
Db 391 CEFLMQALQSLQNMELQLAQLTEK 415

RESULT 3

T16973 tobacco (curled-leaved tobacco)
C:Species: *Nicotiana plumbaginifolia* (curled-leaved tobacco)
C:Accession: T16973
R:Hudson, M. B.; Robson, P.R.H.; Kraepiel, Y.; Caboche, M.; Smith, H.
A:Title: *Nicotiana plumbaginifolia* h19 mutants have a mutation in a PHYB-type phytochrom
A:Reference number: Z16826; PMID:9418050
A:Status: preliminary; translated from GB/EMBL/DDJB
A:Molecule type: DNA
A:Residues: 1-1135 <WUD>
A:Experimental source: cultivar PBH1; leaf
C:Genetics:
C:Superfamily: phytochrome, conventional type; phytochrome homology
F:32-592/Domain: phytochrome homology <PHY>
F:338/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match Score 836; DB 2; Length 1135;
Best Local Similarity 77.0%; Pred. No. 2.3e-74;
Matches 157; Conservative 18; Mismatches 21; Indels 8; Gaps 1;

Qy 1 KLAVALRISLQLSPCGDVLCDTVDYQRLTGDRWVYQFEDDHGEVSEIRSDL 60
Db 217 KLAVALRISLQLSPCGDVLCDTVDYQRLTGDRWVYKFEDHEGEVSEIRSDL 276

RESULT 4

T03668 common tobacco
C:Species: *Nicotiana tabacum* (common tobacco)
C:Accession: T03668; T03672
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
R:Kern, R.; Gasic, A.; Deak, M.; Kay, S.A.; Chua, N.H.
A:Title: PhyB of tobacco, a new member of the photoreceptor family.
A:Reference number: Z14996; PMID:94105358; PMID:8278560
A:Accession: T03668
A:Status: preliminary; translated from GB/EMBL/DDJB
A:Molecule type: DNA
A:Residues: 1-1132 <WER>
A:Cross-references: UNIPROT:P29130; UNIPARC:UPI0000131A67; EMBL:L10114; PMID:9295345; PID
A:Experimental source: strain SRL; tissue-type etiolated seedling
R:Alvarez-Juez, E.; Nagatani, A.; Tomizawa, K.; Deak, M.; Kern, R.; Kendrick, R.E.; Furuya, A.; Reference number: Z14997; PMID:92361250; PMID:198594
A:Title: The cucumber long hypocotyl mutant lacks a light-stable PHYB-like phytochrome.
A:Accession: T03672
A:Status: preliminary; translated from GB/EMBL/DDJB
A:Molecule type: mRNA
A:Residues: 457-505; 'S', '508-586,'Q', '587-1132 <LOP>
A:Cross-references: UNIPARC:UPI000016D893; EMBL:M65023; PMID:9170286; PMID:AAA34093.1; PMID:91237083
C:Genetics:
A:Gene: phyB
C:Superfamily: phytochrome, conventional type; phytochrome homology
C:Keywords: chromoprotein; photoreceptor; phytochromobilin
P:80-589/Domain: phytochrome homology <PHY>
P:336/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match Score 828; DB 2; Length 1132;
Best Local Similarity 76.5%; Pred. No. 1.4e-17;
Matches 156; Conservative 18; Mismatches 22; Indels 8; Gaps 1;

Qy 1 KLAVALRISRLQSLPGDIGALCDTVDYQRLTGDRWVYQFEDDHGEVSEIRSDL 60
Db 215 KLAVALRISLQLSPCGDVLCDTVDYQRLTGDRWVYKFEDHEGEVSEIRSDL 274
Qy 61 EPYLGLHYPATDIPQAARFLFKONVRMIDCNATPVQVOSBELKRPCLVNSTRAPL 120
Db 275 EPYLGLHYPATDIPQAARFLFKONVRMIVDCHATPVQVOSBELMOPCLVGSTPSAPL 334
Qy 121 GCHTOQMAMGVSASLAIIVVKGD-----SSKLWGLVGHCSPRYVPPFLRYA 196
Db 335 GCHQYQMAMGTSRSLMAVITNGNDDEGGSGRNSMKLWGLVYVCHHTSPRAVPPFLRYA 394
Qy 173 EFLMQAFGLQLOMELQASLQAK 196
Db 395 EFLMQALQSLQNMELQLAQLTEK 418

RESULT 5

T14802 sorghum (fragment)
C:Species: Sorghum bicolor (sorghum)
C:Accession: T14802
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
R:Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mullet,

submitted to the EMBL Data Library, April 1996
 A;Description: The *Sorghum bicolor* photoperiod sensitivity gene, *Ma3*, encodes a phytochrome

A;Accession: T14802
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
 A;Residues: 1-1039 <CYS>

A;Cross-references: UNIPARC:UPI0000174B16; EMBL:U56730; PID:91800216

A;Experimental source: cultivar 58M

C;Genetics:
 A;Gene: PHYB

A;Note: Intron positions not resolved (incomplete sequence)

C;Superfamily: phytochrome, conventional type; phytochrome homology
 C;Keywords: chromoprotein; photoreceptor; phytochromobilin (Cys) (covalent) #status predicted

F;233/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 78.4%; Score 802.5; DB 1; Length 1172;

Best Local Similarity 72.9%; Pred. No. 5e-71; Mismatches 22; Indels 11; Gaps 1;

Matches 151; Conservative 23; MisMatches 21; Gaps 1;

Query Match 78.7%; Score 806; DB 2; Length 1039;

Best Local Similarity 73.6%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

Query Match 61 EPIGLHYPATDIPQAARPLFKONVRMTCDCNATPVRKVQSEBLKRPCLVNSTRAPL 60

Best Local Similarity 70.4%; Pred. No. 2e-71; Mismatches 21; Indels 12; Gaps 2;

Matches 153; Conservative 21; MisMatches 22; Indels 12; Gaps 2;

RESULT 8

S62714 phytochrome 1b - *Mesotaenium caldarium*
 C:Species: *Mesotaenium caldarium*
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
 C:Accession: S62714
 R:Lagarrias, D.M.; Wu, S.H.; Lagarias, J.C.
Plant Mol. Biol. 29, 1127-1142, 1995
 A:Title: Atypical phytochrome gene structure in the green alga *Mesotaenium caldarium*.
 A:Reference number: S62713; PMID:96191280; PMID:8616213
 A:Accession: S62714
 A:Molecule type: DNA
 A:Residues: 1-1142 <LAG>
 A:Cross references: UNIPROT:Q40263; UNIPARC:UPI000009D253; EMBL:U31284; NID:g1125698; PI
 A:Intitrons: 125/1: 298/3: 393/3: 468/3: 543/2: 621/3: 699/1: 785/1: 856/3: 970/2: 1067/2
 C:Superfamily: phytochrome, conventional type; phytochrome homology
 C:Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription regulation
 P:68-589/Domain: phytochrome homology <PHY>
 P:880-1139/Domain: signal transduction #status Predicted <STD>
 P:324/Binding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match 1 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 120
 Best Local Similarity 71.2%; Pred. No. 4.3e-19; Score 783; DB 2; Length 1164;
 Matches 148; Conservative 24; Mismatches 24; Indels 12; Gaps 1;

Db 239 KLAVALSHLQSLPQASRLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 60
 Query Match 1 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 120
 Best Local Similarity 71.2%; Pred. No. 4.3e-19; Score 783; DB 2; Length 1164;
 Matches 148; Conservative 24; Mismatches 24; Indels 12; Gaps 1;

Db 239 KLAVALSHLQSLPQASRLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 60
 Query Match 1 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 120
 Best Local Similarity 70.0%; Pred. No. 2.6e-69; Score 785; DB 2; Length 1142;
 Matches 147; Conservative 20; Mismatches 29; Indels 14; Gaps 1;

Db 203 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 60
 Query Match 1 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 120
 Best Local Similarity 70.0%; Pred. No. 2.6e-69; Score 785; DB 2; Length 1142;
 Matches 147; Conservative 20; Mismatches 29; Indels 14; Gaps 1;

Db 263 EPIGLHYPATDIPQAARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 322
 Query Match 1 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 120
 Best Local Similarity 70.0%; Pred. No. 2.6e-69; Score 785; DB 2; Length 1142;
 Matches 147; Conservative 20; Mismatches 29; Indels 14; Gaps 1;

Db 323 GCHQYMANMGSVASLVMVPPINNSSEGGATAAGGILHGRKLWGLYVCHSSPRVYP 382
 Query Match 1 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 120
 Best Local Similarity 70.0%; Pred. No. 2.6e-69; Score 785; DB 2; Length 1142;
 Matches 147; Conservative 20; Mismatches 29; Indels 14; Gaps 1;

Db 383 PLRACEFIMQAFGLQMLNEMQLAQSEK 412
 RESULT 9

B71429 phytochrome D - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Variety: columba
 C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 31-Dec-2004
 C:Accession: B71429; S41910
 R:Devan, M.; Bancroft, I.; Bent, B.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
 avanagh, T.; Hembel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
 P:Weiler, E.; Wedler, R.; Wambutt, R.; Weitznecker, T.; Pohl, T.M.; Terry, N.; Giel
 erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
 C.; Chalwatzi, N.
 A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis* that
 A:Cross-references: UNIPROT:F42497; UNIPARC:UPI0000131A6A; GB:92244950; PIDN
 R;Clack, T.; Mathews, S.; Sharrock, R.A.
Plant Mol. Biol. 25, 413-427, 1994
 A:Title: The phytochrome apoprotein family in *Arabidopsis* is encoded by five genes: the
 A:Reference number: S44312; PMID:94325466;
 A:Accession: S44312
 A:Molecule type: DNA
 A:Residues: 1-424 'F' 426-1164 '<GLA>'
 A:Cross-references: UNIPARC:UPI000016DBB1; EMBL:X76609; NID:g452812; PIDN:CAA54072.1; PI
 C:Genetics:
 A:Gene: PhyB

Query Match 1 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 63
 Best Local Similarity 72.6%; Pred. No. 5.2e-68; Score 772; DB 2; Length 1156;
 Matches 146; Conservative 20; Mismatches 27; Indels 8; Gaps 1;

Db 240 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 63
 Query Match 1 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 63
 Best Local Similarity 72.6%; Pred. No. 5.2e-68; Score 772; DB 2; Length 1156;
 Matches 146; Conservative 20; Mismatches 27; Indels 8; Gaps 1;

Db 300 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 63
 Query Match 1 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 63
 Best Local Similarity 72.6%; Pred. No. 5.2e-68; Score 772; DB 2; Length 1156;
 Matches 146; Conservative 20; Mismatches 27; Indels 8; Gaps 1;

Db 360 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 63
 Query Match 1 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 63
 Best Local Similarity 72.6%; Pred. No. 5.2e-68; Score 772; DB 2; Length 1156;
 Matches 146; Conservative 20; Mismatches 27; Indels 8; Gaps 1;

Db 420 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 63
 Query Match 1 KLAVALRSRLQSLPQARFLPKNRVYRMCIDCNATPVKVYQSEELKRPLCLVNSTLRAPH 63
 Best Local Similarity 72.6%; Pred. No. 5.2e-68; Score 772; DB 2; Length 1156;
 Matches 146; Conservative 20; Mismatches 27; Indels 8; Gaps 1;

RESULT 11

A; Cross-references: UNIPARC:UPI000174E20
 C; Genetics:
 A; Introns: 686/1; 959/2; 1056/2
 C; Superfamily: phytochrome, conventional type; phytochrome homology
 C; Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription regulation
 P; 66-582/Domain: phytochrome homology <phyt>
 F; 324/Banding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match, Score 72.9%; DB 2; Length 1134;
 Best Local Similarity 67.9%; Pred. No. 1.5e-65;
 Matches 142; Conservative 23; Mismatches 30; Indels 14; Gaps 2;
 Db 1 KLAVALISLQLSPLGGDTGALCDTVDVQRLGTYDRMVYQHEDDHGEVSEIRSDL 60
 Db 203 KLAAKAISLQLSPGGDGLLCLDTVVERDVTGDLVMAKPHEDHEGEVVAEIRSDL 262
 Qy 61 EPIGLHYPATDIPQAARLFLFKQNVRMIDCNATPVKVOSEBLKRPLCLVNSTLRAPH 120
 Db 263 EPIGLHYPATDIPQAARLFLFKQNVRMIDCNATPVKVOSEBLKRPLCLVNSTLRAPH 322
 Qy 121 GCHTOYMANMGSTASLALIVVKGKD-----SSKLWGLVYGHHCSPRYVPP 167
 Db 323 GCHAQYMGNGSTASLYNAMITINDEPSGGGGGGKGRRLWGLVCHHTSPRSVPPF- 381
 Qy 168 RYACEFLMAGFGLQLOMELQLASLQAEK 196
 Db 382 LRSACEFLMAGFGLQASLQAEVAVAHREK 410

RESULT 15
 T09496
 Phytochrome - Douglas fir (fragment)
 C; Species: *Pseudotsuga menziesii* (Douglas fir)
 C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
 C; Accession: T09496
 R; Marshall, K.A.; Neale, D. B.
 submitted to the EMBL Data Library, March 1995
 A; Reference number: Z16697
 A; Accession: T09496
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-368 <MAR>
 A; Cross-references: UNIPROT:Q40917; UNIPARC:UPI0000A3684; EMBL:U22458; NID:9726314; PID
 C; Superfamily: phytochrome, conventional type; phytochrome homology
 C; Keywords: chromoprotein; photoreceptor; phytochromobilin
 F; 244/Banding site: phytochromobilin (Cys) (covalent) #status predicted

Query Match, Score 72.9%; DB 2; Length 368;
 Best Local Similarity 66.8%; Pred. No. 5e-66;
 Matches 139; Conservative 22; Mismatches 35; Indels 12; Gaps 1;
 Db 1 KLAVALISLQLSPLGGDTGALCDTVDVQRLGTYDRMVYQHEDDHGEVSEIRSDL 60
 Db 123 KLAAKAISLQLSPGGDGLLCLDTVVERDVTGDLVMAKPHEDHEGEVSEIRSDL 182
 Qy 61 EPIGLHYPATDIPQAARLFLFKQNVRMIDCNATPVKVOSEBLKRPLCLVNSTLRAPH 120
 Db 183 EPIGLHYPATDIPQAARLFLFKQNVRMIDCNATPVKVOSEBLKRPLCLVNSTLRAPH 242
 Qy 121 GCHTOYMANMGSTASLALIVVKGKDSS-----KLGWGLVYGHHCSPRYVPPF 168
 Db 243 GCHAQYMGNGSTASLYNAMITINDEPSGGGGGGKGRRLWGLVCHHTSPRSVPPF 302
 Qy 169 RYACEFLMAGFGLQLOMELQLASLQAEK 196
 Db 303 RYACEFLMAGFGLQASLQAEVAVAHREK 330